

QY	1	Met	Arg	Arg	Phe	Leu	Leu	Leu	Tyr	Ala	Thr	Gln	Gln	Gly	Gln	Ala	lys	Ala	Ile	Ala	Glu	20	
Db		1	ATG	AGG	AGG	TTT	CTG	TACT	TAT	ATG	CTT	AC	CAG	CAG	AGG	GAC	AGG	CA	AGG	CCAT	CTC	CGA	60

```
Qy 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgArg 400
|||
Db 1141 AAAAGGCATTTTGGAGCCCTTGTGACTATACCACTGACAGTCTGAAAAGCCAGG 1200
|||
Qy 401 LeuGlnGluLeuCysSerLysGlnGluAlaAspTyrSerArgPheValArgAspAla 420
|||
Db 1201 CTACAGAGCTGTGAGTAAACAGAGGACCCGATATAGCCGCTTGTACGAGATGCC 1260
|||
Qy 421 CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
|||
Db 1361 TGTGCTGTCTTGTGTGATCTCTCTGCTTTCCTCTTCCCTTGTGCCAGCCACCTCAGTCTC 1320
|||
Qy 441 LeuLeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
|||
Db 1321 CTGCTCGAATCTTCTTAACTTCAACCCAGACCATATTCTGTGTCAGCTCAAGTTTA 1380
|||
Qy 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
|||
Db 1381 TTTACCCAGGAAGCTCTCTTTTGTCTCAACATTTGGAATTTCTGCTACTGCCACA 1440
|||
Qy 481 ThrGluValLeuArgLysGlyValCysThrGlyTrpLeuAlaLeuLeuValAlaSerVal 500
|||
Db 1441 ACAGAGGTTCTCGGAAGGGAGTATGTACAGGCTGGCTGTGCTTGTGTGCTTCAGTT 1500
|||
Qy 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
|||
Db 1501 CTTCAGGCAACATACATGCTATCCATGACAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
|||
Qy 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspSerProSerIleProIle 540
|||
Db 1561 TCCATCTCTCCCTCGAACACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCCATC 1620
|||
Qy 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
|||
Db 1621 ATAATGGTGGTCCAGGAACCGCATAGCCCGTTTATTGGGTCTCTACAACATAGAGAG 1680
|||
Qy 561 LysLeuGlnGluHisProAspGlyAsnPheGlyAlaMetTrpLeuPhePheGlyCys 580
|||
Db 1681 AAACCTCAGAACACACCCAGATGGAAATTTGGAGCAATGGTGTGTTTTTGGCTGC 1740
|||
Qy 581 ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGly 600
|||
Db 1741 AGGCATAAGGATAGGATTTATCTATTCAAGAAAGAGCTCAGACATTTCTTAAAGCATGG 1800
|||
Qy 601 IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAla 620
|||
Db 1801 ATCTTAACATCTAAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGGAGGAAGCC 1860
|||
Qy 621 ProAlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnGlnValAlaArgIleLeu 640
|||
Db 1861 CCAGCAAAAGTATGTACAAGACAACTCCAGCTTACGCCAGCAGGTGGCGAGAATCCTC 1920
|||
Qy 641 LeuGlnGluAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspVal 660
|||
Db 1921 CTCAGGAGAACCGCCATATTTATGTGTGGAGATGCAAGAAATATGGCCAAGGATGA 1980
|||
Qy 661 HisAspAlaLeuValGlnIleLeuSerLysGluValGlyValGluLysLeuGluAlaMet 680
|||
Db 1981 CATGATGCCCTTGTGCAATAATAAGCAAGAGGTGGAGTTGAAAACTAGAACCAATG 2040
|||
Qy 681 LysThrLeuAlaThrLeuLysGluLysArgTyrLeuGlnAspIleTrpSer 698
|||
Db 2041 AAAACCTGSCCACTTAAAGAGAGAAAACGCTACCTTCAGGATATTTGGTCA 2094
|||
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Search completed: December 12, 2002, 08:24:13
Job time : 6 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 12, 2002, 08:25:56 ; Search time 2 Seconds
(without alignments)
1.464 Million cell updates/sec

Title: us-09-371-347a-42

Perfect score: 3623
Sequence: 1 MRRLLLYATQGOAKIAE.....AMKTLATLKEKRYLQDIWS 698

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1 seqs, 2097 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:
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-SUFFIX=ptc -OUT=align_42_41 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTENT=ptc
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NPU=6 -NO_XLPY
-NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : us-09-371-347a-41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3623	100.0	2097	1	us-09-371-347a-41

ALIGNMENTS

RESULT 1
us-09-371-347a-41

Alignment Scores:

Pred. No.:	0	Length:	2097
Score:	3623.00	Matches:	698
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

us-09-371-347a-42 (1-698) x us-09-371-347a-41 (1-2097)

Qy	1	MetArgPheLeuLeuTyrAlaThrGlnGlnGlyAlaLysAlaLeuGlu	20
Db	1	ATGAGGAGGTTTCTGTACTATATGCTACAGCAGGACAGGCAAGGCGCCAGAA	60

Qy	21	GluIleCysGluGlnAlaValValHisGlyPheSerAlaAspLeuHisCysIleSerGlu	40
Db	61	GAATATGTCGAGCAAGCTGTGGTACATGGATTTCCTGCAGATCTTCCTGATTAGTGA	120
Qy	41	SerAspLysTyrAspLeuLysThrGluThrAlaProLeuValValValSerThrThr	60
Db	121	TCCGATAAGTATGACCTAAACACCGAAACAGCTCCTCTGTTGTTGTTGTTTACACG	180
Qy	61	GlyThrGlyAspProProAspThrAlaArgLysPheValLysGluIleGlnAsnGlnThr	80
Db	181	GGCACCAGAGACCCACCGCACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA	240
Qy	81	LeuProValAspPheAlaHisLeuArgTyrGlyLeuGlyLeuGlyAspSerGlu	100
Db	241	CTGCCGGTTGATTCTTGTCTACCTGCGGTATGGGTACTGGGTCTCGGTGATTTCAGAA	300
Qy	101	TyrThrTyrPheCysAsnGlyGlyLysIleAspLysArgLeuGlnGlnGlyAla	120
Db	301	TACACCTACTTTTGCATATGGGGGGAAGATAATTGATAAAGACATTTCAAGAGCTTGGAGCC	360
Qy	121	ArgHisPheTyrAspThrGlyHisAlaAspCysValClyLeuGluLeuValValGlu	140
Db	361	CGGCATTTCTATGACACTGGACATGCAGATGACTGTGTAGTTTAGAACTTGTGCTGAG	420
Qy	141	ProThrIleAlaGlyLeuTyrProAlaLeuArgLysHisPheArgSerArgGlyCln	160
Db	421	CCGTGGATTGCTGGACTCTGCCAGCCCTCAGAAAGCATTTTAGGTCAAGCAGAGGACAA	480
Qy	161	GluGluIleSerGlyAlaLeuProValAlaSerProAlaSerLeuArgThrAspLeuVal	180
Db	481	GAGGAGATAAGTGGCGCACTCCCGTGGCATCACCTGCATCTTCAGGACAGACCTTGTG	540
Qy	181	LysSerGluLeuLeuHisIleGlySerGlnValGluLeuLeuArgPheAspAspSerGly	200
Db	541	AGTCAAGCTGCTACACATTTGAATCTCAAGTTCGACTCTCGATTCGATGATTTCAGGA	600
Qy	201	ArgLysAspSerGluValLeuLysGlnAsnAlaValAsnSerAsnGlnSerAsnVal	220
Db	601	AGAAAGGATTCTGAGGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAAATGTTGA	660
Qy	221	IleGluAspPheGlySerLeuThrArgSerValProLeuSerGlnAlaSerLeu	240
Db	661	ATTGAAGACTTTTGAGTCTCTACTTTACCGTTCGGTACCCCTCTCTCAAGCCTCTCTG	720
Qy	241	AsnIleProGlyLeuProGlyTyrLeuGlnValHisLeuGlnGlnSerLeuGlyCln	260
Db	721	ATATTCCTGGTTTACCCCAAGATATTTACAGTACATCTCAGGAGTCTCTTGGCCAG	780
Qy	261	GluGluSerGlnValSerValThrSerAlaAspProValPheGlnValProIleSerLys	280
Db	781	GAGGAAAGCAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGAGTCCCAATTTCAAAG	840
Qy	281	AlaValGlnLeuThrThrAsnAspAlaIleLysThrThrLeuLeuValGluLeuAspIle	300
Db	841	GCAGTTCAACTTACTACGAATGATGCCATAAANAACACTCTCTGCTGGTAGAATTGGACAT	900
Qy	301	SerAsnThrAspPheSerTyrGlnProGlyAspAlaPheSerValIleCysProAsnSer	320
Db	901	TCAATATACAGACTTTTCTCTATCAGCCTGGAGATGCCCTTCAGCGTGATCTGCCCTAACAGT	960
Qy	321	AspSerGluValGlnSerLeuGlnArgLeuGlnLeuGluAspLysArgGluHisCys	340
Db	961	GATTCCTGAGGTACAAAGCCTACTCCAAAGACTGCAGCTTGAAGATAAAGAGAGCAGCTGC	1020
Qy	341	ValLeuLeuLysIleLysAlaAspThrLysLysGlyAlaThrLeuProGlnHisIle	360
Db	1021	GTCCTTTTGAAATAAAGCGACACAAAGAAAGAGGAGCTACCTTACCCAGCATATA	1080
Qy	361	ProAlaGlyCysSerLeuGlnPheIlePheThrTrpCysLeuGluIleArgAlaIlePro	380
Db	1081	CCTGGGGATGTTCTCTCCAGTTTCATTTTACCTGGTGTCTTGAATCCGAGCAATTCCT	1140

```
Qy 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgAtg 400
Db 1141 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Qy 401 LeuGlnLeuLysSerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla 420
Db 1201 CTACAGAGCTGTGCAGTAACAAAGGGCAGCCGATTATAGCCGCTTTGTACGAGATGCC 1260
Qy 421 CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
Db 1261 TGTGCTGTCTGTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Qy 441 LeuLeuGlnHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
Db 1321 CTGCTGAACATCTTCTAACTTCAACCCAGACCATATCTGTGCAAGCTCAAGTTTA 1380
Qy 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
Db 1381 TTTCAACCCAGGAAGCTCCATTTCTCTTCAACATTTGGAAATTTCTGTCTACTGCCACA 1440
Qy 481 ThrGluValLeuArgLysGlyValCysThrGlyTrpLeuAlaLeuValAlaSerVal 500
Db 1441 ACAGAGGTTCTCGGAAGGAGATGTACAGCTGGCTGGCTTGTGGTGTGCTTGTGCTT 1500
Qy 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
Db 1501 CTTCAAGCAACATACATCCATCCATGAACACAGCGGAAGCCCTGGCTCCTTAAGATA 1560
Qy 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
Db 1561 TCCATCTCTCTCGAACAATAATCTTTCCACTTACCAGATGACCCCTCAATCCCCATC 1620
Qy 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
Db 1621 ATATGCTGGTCCAGAACCCGGCATAGCCCGTTTATGGGTTCCTACACATAGAGAG 1680
Qy 561 LysLeuGlnGluGlnHisProAspGlyAsnPheGlyAlaMetTrpLeuPhePheGlyCys 580
Db 1681 AAATCCAAAGAACACCCAGATGGAAATTTTGGAGCAATGTGGTGTGTTTTTGGCTGC 1740
Qy 581 ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGly 600
Db 1741 AGGCATAAGCATAGGCATTATCTATTACAAAAGAGCTCACACATTTCTTAAAGCATGG 1800
Qy 601 IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAla 620
Db 1801 ATCTAACTCATCTAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGGAGGAGCC 1860
Qy 621 ProAlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnValAlaArgIleLeu 640
Db 1861 CCAGCAAAAGTATGTACAAGACAACATCCAGCTTCATGCCAGCAGGTGGCGAGAACTCCTC 1920
Qy 641 LeuGlnGluAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspVal 660
Db 1921 CTCCAGGAGAACCGCCATATTATGTGTGGAGATGCCAAGAATATGGCCAGGATGTA 1980
Qy 661 HisAspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGluAlaMet 680
Db 1981 CATGATGCCCTTGTGCAATAATTAAGCAAGAGGTTGGAGTTGAAAACTAGAACCAATG 2040
Qy 681 LysThrLeuAlaThrLeuLysGluLysArgTyrLeuGlnAspIleTrpSer 698
Db 2041 AAAACCTGGCCACTTTTAAAGAAGAAACCCCTACCTTCAGGATATTGGTCA 2094
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Search completed: December 12, 2002, 08:26:03
Job time : 7 secs

GenCore version 5.1.3
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OM protein - nucleic search; using frame_plus_p2n model

Run on: December 12, 2002, 08:27:12 ; Search time 2 Seconds

(without alignments)
1.464 Million cell updates/sec

Title: us-09-371-347a-44
 Perfect score: 3620
 Sequence: 1 MRRFLLLYATQGOAKAIAE.....AMKTLATLKEEKRYLQDINS 698

Scoring table:	BLASUM62		
	Xgapop	10.0	Xgapext 0.1
	Ygapop	10.0	Ygapext 0.1
	Fgapop	6.0	Fgapext 0.1
	Delop	6.0	Delext 0.1

Searched: 1 seqs, 2097 residues

Total number of hits satisfying chosen parameters: 2

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
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 SUFFIX=none-20000144
 MINMATCH=0 L=LOCAL LCOREY=0 UNITS=bis
 START=1 END=1 MATHY=635252 TRANS=huma40 cdi LIST=1 LOCALCN=200
 THRESHOLD=1
 NORM=oct THIR MAX=100 THR_MIN=0 MODE=LOCAL OUTPMT=pto
 SCORE=1 HEADSIZE=500 MINLEN=0 MAXLEN=200000000 NCPU=6 NO_XLPHY
 NEG_SCORES=0 LONGLOC THREADS=1 XGAPOP=10 XGAEXT=0 FGAPOP=6
 FGAPXT=0 YGAPOP=10 YGAEXT=0 DELOP=6 DELEXT=0

Database : us-09-371-347a-43:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3613	99.8	2097	1	us-09-371-347a-43

ALIGNMENTS

RESULT 1
US-09-371-3478-43

Alignment Scores:		
Pred. No.:	0	Length: 2097
Score:	3613.00	Matches: 697
Percent Similarity:	99.86%	Conservative: 0
Best Local Similarity:	99.86%	Mismatches: 1
Query Match:	99.81%	Indels: 0
DB:	1	Gaps: 0

us-09-371-347a-44 (1-698) x us-09-371-347a-43 (1-2097)

QY	1	Met	Arg	Arg	Phe	Leu	Leu	Tyr	Ala	Thr	Gln	Gln	Gly	Gln	Ala	Lys	Ala	Ile	Ala	Glu	20
D6	1	ATG	AGG	AGG	TTT	CTG	TACT	TAT	ATG	CTA	ACG	AGG	AGG	CAAG	GGCC	ATCG	CAG	AA	60		

```
QY 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArg 400
Db 1141 AAAAAGGCATTTTTCGAGGCCCTTGTGGACTATACAGTGCACAGTGTCTAAAAGCCAGG 1200
QY 401 LeuGlnGluLeuCysSerLysGlnGlyValAlaAspTyrSerArgPheValArgAspAla 420
Db 1201 CTACAGGAGCTGTGCAGTAAACAGGGCCAGCCGATTAAGCCGCTTTGTACGAGATGCC 1260
QY 421 CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
Db 1261 TGTGGCTGCTTGTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 441 LeuLeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
Db 1321 CTGCTCGAACATCTTCCCTAACTTCAACCCAGACCATATTCTGTCGCAAGCTCAAGTTTA 1380
QY 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
Db 1381 TTTCACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACA 1440
QY 481 ThrGluValLeuArgLysGlyValCysThrGlyTrpLeuAlaLeuValAlaSerVal 500
Db 1441 ACAGAGGTTCTCGGAAGGAGTATGTACAGGCTGGCTGGCCCTTGTGGTCTTCAGTT 1500
QY 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerClyLysAlaLeuAlaProLysIle 520
Db 1501 CTTACGCCAANACTACATGCATCCATGACAGACAGCGGAAAGCCCTGGCTCTAAGATA 1560
QY 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
Db 1561 TCCATCTCTCTCTCGAACACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCCATC 1620
QY 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
Db 1621 ATAATGGTGGGTCCAGGAACCGCATAGCCCGTTTATTGGTTCCTACAACATAGAGAG 1680
QY 561 LysLeuGlnGluHisProAspGlyAsnPheClyAlaMetTrpLeuPhePheGlyCys 580
Db 1681 AACTCCAAAGAACACACCCAGATGGAAATTTGGAGCAATGGTGTGTTTTTGGCTGC 1740
QY 581 ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGly 600
Db 1741 AGGCATAAGGATAGGGATTATCTATTAGAAAAGAGCTCAGACATTTCTTAAAGCATGGG 1800
QY 601 IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAla 620
Db 1801 ATCTTAACATCATCTAAGGTTTCTTCTCAAGAGATGCTCTCTGGGAGGAGGAGGCC 1860
QY 621 ProAlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnValAlaArgIleLeu 640
Db 1861 CCAGCAAGATATGTACAAGACAAACATCCAGCTTCATGCCAGCAGGTGGCGAGAATCCTC 1920
QY 641 LeuGlnGluAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspVal 660
Db 1921 CTCAGGAGACGGCCATATTATCTGTGTGGAGATCCAAAGATATGGCCAGGATGTA 1980
QY 661 HisAspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGluAlaMet 680
Db 1981 CATGATGCCCTTGTGCAAAATAAAGCAAGAGGTTGGAGTTGAAAACCTAGAACCAATG 2040
QY 681 LysThrLeuAlaThrLeuLysGluLysArgTyrLeuGlnAspIleTrpSer 698
Db 2041 AAAACCTGGCCACTTAAAGAGAAAAACGCTACCTTCAGGATATTTGGTCA 2094
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Search completed: December 12, 2002, 08:27:19
Job time : 7 secs


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Qy 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArg 400
Db 1141 AAAAAAGGCATTTTTCGAGCCCTTGTGGACTATACAGTGCACAGTCTCAAAAAGCCAGG 1200
Qy 401 LeuGlnGluLeuCysSerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla 420
Db 1201 CTACAGGAGCTGTGCAGTAAACAGGGGCGAGCGATTATAGCGCTTGTACGAGATGCC 1260
Qy 421 CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
Db 1261 TGTGCTGCTGTTGTGGATCTCTCTCTGCTTTCCTTCTTGCAGCCACCACTCAGTCTC 1320
Qy 441 LeuLeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
Db 1321 CTGCTCGAATCTTCTTAACTTCAACCCAGACCATATTCGNGTCAAGCTCAAGTTTA 1380
Qy 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
Db 1381 TTACACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCCACA 1440
Qy 481 ThrGluValLeuArgLysGlyValCysThrGlyTyrLeuAlaLeuValAlaSerVal 500
Db 1441 ACAGAGGTTCTCGGAAGGGAGTATGACAGGTGGCTGGCTTGTGGTTCCTTCAGTT 1500
Qy 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
Db 1501 CTTACGCCAAACATACATGCATCCATGAGACAGCGGGAACCCCTGGCTCCTAAGATA 1560
Qy 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
Db 1561 TCCATCTCTCTCGAACAACAAATTTCTTCCACTTACAGATGACCCCTCAATGCCCATC 1620
Qy 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
Db 1621 ATAATGGTGGTCCAGGAACCGGATAGCCCGTTTATGGGTTCCTACAACATAGAGAG 1680
Qy 561 LysLeuGlnGluGlnHisProAspGlyAsnPheGlyAlaMetTyrPheGlyCysArg 580
Db 1681 AAATCCCAAGAACACACCCAGATGGAAATTTGGACAAATGGTTTGTGGCTGCAGG 1740
Qy 581 HisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGlyIle 600
Db 1741 CATAAGGATAGGATTTATCTATTTCAGAAAGAGCTCAGACATTTCTTAAAGCATGGATC 1800
Qy 601 LeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAlaPro 620
Db 1801 TTAATCATCTAAGGTTTCTTCTCAAGAGATGCTCTCTTGGGAGGAGGAGGCCCA 1860
Qy 621 AlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnGlnValAlaArgIleLeuLeu 640
Db 1861 GCAAAGTATGTACAAGACAACTCCAGCTTCATGGCCAGCAGGTGGCGAATCTCTCTC 1920
Qy 641 GlnGluAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspValHis 660
Db 1921 CAGGAGAACGGCCATATTTATGTGTGGAGATGCAAGAAATATGGCCAAAGGATGTACAT 1980
Qy 661 AspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGluAlaMetLys 680
Db 1981 GATGCCCTTGTGCAATATATAGCAAGAGGTTGGAGTTGAAAACATAGCAATGAAA 2040
Qy 681 ThrLeuAlaThrLeuLysGluLysArgTyrLeuGlnAspIleTyrSer 697
Db 2041 ACCCTGGCCACTTTAAAGAAGAAAACGCTACCTTCAGGATATTTGGTCA 2091
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Search completed: December 12, 2002, 08:28:29
Job time : 4 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 12, 2002, 08:29:25 ; Search time 1 Seconds
(without alignments)
2.884 Million cell updates

Title: us-09-371-347a-48
 Perfect score: 3568
 Sequence: 1 RRELLLYATQOGAKAAIEE.....NKOKPWPLKKKNATERIEGH 689

Scoring table:	BLOSUM62				
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	Ygapop	10.0	Ygapext	0.1	
	Fgapop	6.0	Fgapext	0.1	
	Delop	6.0	Delext	0.1	

Searched: 1 seqs, 2093 residues

Total number of hits satisfying chosen parameters: 2

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

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Command line parameters:
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-DEV=soft
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-DBus=09-371-347a-47
-SUFFIX=pc
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-LOOPX=0
-LOOPEXT=0
-UNITS=bits
-START=1
-END=1
-MATRIX=plosum22
-TRANS=human40
-SDI=LIST=1
-LOCAL=200
-THR SCORE=pcr
-THR MAX=100
-THR MIN=0
-ALIGN=1
-MODE=LOCAL
-OUTFILE=pc
-NORM=acc
-HEAPSIZ=500
-MINLEN=0
-MAXLEN=200000000
-NCPU=6
-NO_XLPRX
-NEG SCORES=0
-LONGLOG
-THREADS=1
-XGAPE=10
-XGAPEXT=0
-1_FGAPOP=6
-XGAPEXT=0
-1_YGAPOP=10
-YGAPEXT=0
-1_DELOP=6
-DELEX=0
-1

```

Database : us-09-371-347a-47:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3529.9	98.9	2093	1	us-09-371-347a-47

ALIGNMENTS

RESULT 1
US-09-371-347a-47

Alignment Scores:					
Pred. NO.:	0	Length:	2093		
Score:	329.90	Matches:	689		
Percent Similarity:	97.04%	Conservative:	0		
Best Local Similarity:	97.04%	Mismatches:	0		
Query Match:	98.93%	Indels:	21		
DB:	1	Gaps:	0		

us-09-371-347a-48 (1-689) x us-09-371-347a-47 (1-2093)

Qy 1 ArgArgPheLeuLeuTyrAlaThrGlnGlnGlnGlnGlnGlnGlu 20
 |||||
 Db 4 AGGAGGTTCTGTACTATGTCACAGCAGGGGACAGGC AAAGGGCATCGCAGAGAA 63
 |||||

```
QY 381 LysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgArgLeu 400
    |||||
Db 1144 AAGGCATTTTGGAGCCCTTGTGGACTATACAGTGCAGTGTGAAAGCGCAGGCTA 1203
    |||||
QY 401 GlnGluLeuCysSerLysGlnGlyValAlaAspTyrSerArgPheValArgAspAlaCys 420
    |||||
Db 1204 CAGGAGCTGTGCAGTAACACAGGGCAGCGATATAGCGCTTTGTACGATGCCCTGT 1263
    |||||
QY 421 AlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeuLeu 440
    |||||
Db 1264 GCCTGCTTGTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1323
    |||||
QY 441 LeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeuPhe 460
    |||||
Db 1324 CTCGAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1383
    |||||
QY 461 HisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThrThr 480
    |||||
Db 1384 CACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACAACA 1443
    |||||
QY 481 GluValLeuArgLysGlyValCysThrGlyTrpLeuAlaLeuValAlaSerValLeu 500
    |||||
Db 1444 GAGGTTCTCGGAGGAGTATGACAGGCTGGCTGGCTTGTGTGCTTCACTTCTCT 1503
    |||||
QY 501 GlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIleSer 520
    |||||
Db 1504 CAGCCAAACATACATGATCCATGACAGAGCGGGAAGCCCTGCTCTTAAGATATCC 1563
    |||||
QY 521 IleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIleIle 540
    |||||
Db 1564 ATCTCTCTCTCGAACAAACAAATTTCTTCCACTTACCATGACCCCTCAATCCCATCAT 1623
    |||||
QY 541 MetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgAsnSer 560
    |||||
Db 1624 ATGGTGGGTCTCAGGAACCGCATAGCCCGTTTATTGGGTCTCTACAAACATAGAACTCC 1683
    |||||
QY 561 LysAsnAsnThrGlnMetGluIleLeuGluCysGlyCysPheLeuAlaGlyIle 580
    |||||
Db 1684 AAGAACACACCCCATGATGGAATTTGGAGCAATGGTGTGTTTGGCTGCAGGCATA 1743
    |||||
QY 581 ArgIleGlyIleIleTyrSerGluLysSerSerAspIleSerLeuSerMetGlySer--- 599
    |||||
Db 1744 AGGATAGGGATTTATCTATTAGAAAGAGCTCAGACATTTCTTAAGCATGGGATCTTAA 1803
    |||||
QY 600 LeuIle---ArgPheProSerGlnGluMetLeuLeuLeuGlyArgArgLysProGlnGln 618
    |||||
Db 1804 CTCATCTAAGGTTTCTCTCTCAGAGATGCTCTCTGTGGGAGAGGAGGCCAGCAA 1863
    |||||
QY 619 SerMetTyrLysThrThrSerSerPheMetAlaSerArgTrpArgLysSerSerArg 638
    |||||
Db 1864 AGTATGTACAGACAAACATCCAGCTTTCATGGCCAGCAGGTGGCGGAGAACTCTCTCCAGG 1923
    |||||
QY 639 ArgThrAlaIlePheMetCysValGluMetGlnArgIleTrpProArgMetTyrMetMet 658
    |||||
Db 1924 AGAACGGCCATATTATGTGTGTGGAGATGCAAGAAATATGGCCAGGATGTACATGATG 1983
    |||||
QY 659 ProLeuCysLys-----AlaLysArgLeuLeuLysAsn---LysGln---LysPro 674
    |||||
Db 1984 CCCTTGTGCAATAATAAGCAAGAGGTGGAGTTGAAGAACTAGAGCAATGAAGAACCC 2043
    |||||
QY 675 TrpProLeu---LysLysLysAsnAlaThrPheArgIlePheGlyHis 689
    |||||
Db 2044 TGCCCACTTTAAAGAGAAAGAACGCTACCTTCAGGATATTGGTCAAT 2091
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Search completed: December 12, 2002, 08:29:31
Job time : 6 secs